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Computer analysis of complete prokaryotic genomes shows that microbial proteins are in general highly conserved--approximately 70% of them contain ancient conserved regions. This allows us to delineate families of orthologs across a wide phylogenetic range and, in many cases, predict protein functions with considerable precision. Sequence database searches using newly developed, sensitive algorithms result in the unification of such orthologous families into larger superfamilies sharing common sequence motifs. For many of these superfamilies, prediction of the structural fold and specific amino acid residues involved in enzymatic catalysis is possible. Taken together, sequence and structure comparisons provide a powerful methodology that can successfully complement traditional experimental approaches.

## Publication Types:

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